## SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals s.a.

<120> Novel Compounds

<130> B45282

<160>26

<170> FastSEQ for Windows Version 4.0

<210>1

<211>909

<212> DNA

<213> Dermatophagoides pteronyssinus

<220>

<221> CDS

<222>(1)...(906)

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aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20

25

30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser 

gee gag get tte gaa cae ett aag ace eag ttt gat ete aac geg gag 240 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu 

ace aac gee tge agt ate aac gge aat gee eec get gag att gat etg 288 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu 

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly 

tet tgt tgg gee ttt tea gge gtg gee geg aca gag teg gea tac etc 384 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp 

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr 

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180

185

190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195

200

205

gag gee etg geg eag aeg eac age gee ate get gte ate ate gga ate 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210

215

220

aag gat etg gac gea tte egg eac tat gae ggg ege aca ate ate eag 720 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac teg aac gee eag ggg gtg gac tac tgg ate gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp IIe Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa

909

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Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu <210>3 <211>302 <212> PRT <213> Artificial Sequence <220> <223> C4R mutant of ProDer p 1 <400>3 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 12:

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg

195 200 205

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210 215 220

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225 230 235 240

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

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<213> Artificial Sequence

<220>

<221> CDS

<222>(1)...(906)

<223> C4R mutant of ProDer p 1

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Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe 20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His 35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct tte gaa cac ett aag ace cag ttt gat ete aac gcg gag 240 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu 65 70 75 80

acc aac gcc cgt agt atc aac ggc aat gcc ccc gct gag att gat ctg 288

Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att toe aat tat tge eag ate tae eee eet aat gee aac aag ate agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 210 215 220

aag gat etg gae gea tte egg eac tat gae ggg ege aca ate ate eag 720 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210>5

<211>302

<212> PRT

<213> Artificial Sequence

<220>

<223> C31R mutant of ProDer p 1

<400> 5

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

5 10

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

15

20 25 30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 125 · Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu 

<210>6

<211>909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222>(1)...(906)

<223> C31R mutant of ProDer p 1

<400>6

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cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

aag agc tat gee ace tte gag gae gag gae gee gee ege aag aac tte 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

55

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

60

gcc gag gct tte gaa cac ett aag acc cag ttt gat ete aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc cgt ggg 336 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly

PCT/EP2004/001850

100

105

110

tet tgt tgg gee ttt tea gge gtg gee geg aca gag teg gea tae etc 384 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115

120

125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tee aat tat tge eag ate tae eec eet aat gee aac aag ate agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 210 215 220

aag gat etg gae gea tte egg eac tat gae ggg ege aca ate ate eag 720 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245

250

255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260

265

270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275

280

285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290

295

300

taa

909

<210>7

<211>302

<212> PRT

<213> Artificial Sequence

<220>

<223> C65R mutant of ProDer p 1

<400>7

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5

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Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

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25

30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35

40

45

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg

195 200 205

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210 215 220

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225 230 235 240

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290 295 300

<211>909

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<220>

<221> CDS

<222>(1)...(906)

<223> C65R mutant of ProDer p 1

<400>8

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Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

85

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

90

95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tet tgt tgg gee ttt tea gge gtg gee geg aca gag teg gea tac etc 384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

cgt gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480 Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175

gta get agg gag eag tee tge ege egt eet aac gea eag ege tte gge 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tee aat tat tge eag ate tae eet eat gee aac aag ate agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210>9

<211>302

<212> PRT

<213> Artificial Sequence

<220>

<223> C71R mutant of ProDer p 1

<400>9

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu 

<210> 10

<211>909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222>(1)...(906)

<223> C71R mutant of ProDer p 1

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1

5

10

15

aag age tat gee ace tte gag gae gag gae gee gee gee aag aac tte 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20

25

30

ctg gaa age gtg aaa tac gtg cag age aac gge ggg get ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35

40

45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50

55

60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65

70

75

80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tet tgt tgg gee ttt tea gge gtg gee geg aca gag teg gea tac etc 384 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp 130 135 140

tge gee tee caa cae gga egt eat ggg gat aeg att eee aga ggt ate 480 Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tee aat tat tge eag ate tae eet eat gee aac aag ate agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

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210 215 220

aag gat etg gae gea tte egg eac tat gae ggg ege aca ate ate eag 720 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tog aac goc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 11

<211>302

<212> PRT

<213> Artificial Sequence

<220>

<223> C103R mutant of ProDer p 1

<400> 11

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1	5	10		15			
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe							
	20	25	3	30			
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His							
	35	40	45				
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser							
50	O	55	60				
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu							
65		70	75	80			
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu							
	85	90		95			
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly							
	100	105		110			
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu							
	115	120	12	25			
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp							
13	30	135	140				
Cys	Ala Ser C	in His Gly (	Cys His G	Gly Asp Thr Ile Pro Arg Gly Ile			
145		150	155	160			
Glu	Tyr Ile G	ln His Asn G	ly Val V	al Gln Glu Ser Tyr Tyr Arg Tyr			
	165	17	<b>70</b>	175			
Val Ala Arg Glu Gln Ser Arg Arg Pro Asn Ala Gln Arg Phe Gly							
	180	185		190			
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg							
	195	200	20	05			
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile							
2	10	215	220				
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln							
225		230	235	240			
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly							
	245	25	50	255			
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp							
	260	265		270			
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile							

275 280 285

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290 295 300

<210> 12

<211>909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222>(1)...(906)

<223> C103R mutant of ProDer p 1

<400> 12

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Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag age tat gee ace tte gag gae gag gag gee geg ege aag aac tte 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tet tgt tgg gee ttt tea gge gtg gee geg aca gag teg gea tae etc 384 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175

gta gct agg gag cag tcc cgt cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210

215

220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 13

<211>302

<212> PRT

<213> Artificial Sequence

<220>

<223> C117R mutant of ProDer p 1

<400> 13 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260

265

270

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275

280

285

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290

295

300

<210>14

<211>909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222>(1)...(906)

<223> C117R mutant of ProDer p 1

<400> 14

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1

5

10

15

aag age tat gee ace tte gag gae gag gag gee geg ege aag aac tte 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20

25

30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35

40

45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

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T

50 55

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

60

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tet tgt tgg gee ttt tea gge gtg gee geg aca gag teg gea tac etc 384 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta get agg gag eag tee tge ege egt eet aac gea eag ege tte gge 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

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att tee aat tat egt eag ate tae eee eet aat gee aac aag ate agg 624 Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195

200

205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210

215

220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 240 230 235 225

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly 245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp 265 270 260

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile 285 280 275

906 gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu 290

295

300

909 taa

<210> 15

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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<210> 16

<211>103

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 16

cggatgggag tcacggtcct catctggcgc agatcaatct cagcgggggc attgccgttg 60 atactacggg cgttggtctc cgcgttgaga tcgaaactgg gtc 103

<210>17

<211>92

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

caaggeggee gtgggtettg ttgggeettt teaggegtgg eegegacaga gteggeatae 60 etegegtate ggaateagag eetggaeete ge 92

<210>18

<211>99

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 18

teagegaggt ceaggetetg atteegatae gegaggtatg cegaetetgt egeggeeaeg 60 cetgaaaagg ceeaaeaaga ceeaeggeeg cettgeatg 99

<210> 19

<211>83

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

tgagcaggag ctcgttgacc gtgcctccca acacggatgt catggggata cgattcccag 60 aggtatcgaa tacatccagc ata 83

<210>20

<211>77

<212> DNA

<213> Artificial Sequence

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<223> Primer

<400>20

ctggatgtat tcgatacctc tgggaatcgt atcccccatg acatccgtgt tgggaggcac 60 ggtcaacgcg ctcctgc 77

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29

-0.1	Λ-	01
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<211>29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400>21

actgacaggc ctcggccgag ctccattaa

<210>22

<211>29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400>22

cagtcaccta ggtctagact cgaggggat 29

<210>23

<211>25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400>23

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<210>24

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## WO 2004/076481 <211> 27 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

geteectage taegtategg taatage

<210>25

<211>29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

cctcgcgtat cggcaacaga gcctggacc 29

<210>26

<211>29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

ggtccaggct ctgttgccga tacgcgagg

29

27